

SEQUENCE LISTING

<110> Jegla, Timothy James
ICAgen, Inc.

<120> Kv10.1, a Novel Voltage-Gated Potassium Channel From
Human Brain

<130> 018512-005910US

<140> US 09/833,466

<141> 2001-04-11

<150> US 60/197,793

<151> 2000-04-14

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 2103

<212> DNA

<213> Homo sapiens

<220>

<223> human alpha subunit of voltage-gated potassium
channel Kv10.1

<220>

<221> CDS

<222> (151)..(1788)

<223> Kv10.1

<400> 1

```

ggcaatgtct gagccccctag ctgtgctggt cggggctggc ctctctaaga cagtgcaggc 60
cacgtgatcc atcctcctag aggcagtgag caggtgaggg acccctacca cagccaggag 120
gaaaaagcta ggcgtccact ttccgcagcc atgctcaaac agagtgagag gagacgggtcc 180
tggagctaca ggccctggaa cacgacggag aatgagggca gccaacaccg caggagcatt 240
tgctccctgg gtgcccgttc cggctcccag gccagcatcc acggctggac agagggcaac 300
tataactact acatcgagga agacgaagac ggggaggagg aggaccagtg gaaggacgac 360
ctggcagaag aggaccagca ggcagggggag gtcaccaccg ccaagcccga gggccccagc 420
gaccctccgg cctgtctgtc cacgctgaat gtgaacgtgg gtggccacag ctaccagctg 480
gactactgcg agctggccgg cttcccgaag acgcgcctag gtcgcctggc cacctccacc 540
agccgcagcc gccagctaag cctgtgcgac gactacgagg agcagacaga cgaatacttc 600
ttcgaccgcg acccggccgt cttccagctg gtctacaatt tctacctgtc cgggggtgctg 660
ctgggtgctcg acgggctgtg tccgcgccgc ttcttgagg agctgggcta ctggggcgtg 720
cggctcaagt acacgccacg ctgctgccgc atctgcttcg aggagcggcg cgacgagctg 780
agcgaacggc tcaagatcca gcacgagctg cgcgcgcagg cgcaggtcga ggaggcggag 840
gaactcttcc gcgacatgcg cttctacggc ccgcagcggc gccgcctctg gaacctcatg 900
gagaagccat tctcctcggt ggccgccaa ggcacgcggg tggcgctccag caccttcgtg 960
ctcgtctccg tgggtggcgt ggcgctcaac accgtggagg agatgcagca gcactcgggg 1020
cagggcgagg gcggcccaga cctgcgggcc atcctggagg acgtggagat gctgtgcatg 1080
ggctttttca cgctcgagta cctgctgcgc ctagecctca cgcccgaacct gaggcgcttc 1140
gcgcgcagcg cctcaacct ggtggacctg gtggccatcc tgccgctcta cttcagctg 1200
ctgctcgagt gcttcacggg cgagggccac caacgcggcc agacgggtgg cagcgtgggt 1260
aagggtgggc aggtgttgcg cgtcatgcgc ctcatgcgca tcttccgcat cctcaagctg 1320
gcgcgcact ccaccggact gcgtgccttc ggcttcacgc tgcgccagtg ctaccagcag 1380
gtgggctgcc tgctgctctt catcgccatg ggcattctca ctttctctgc ggctgtctac 1440
tctgtggagc acgatgtgcc cagcaccaac ttactacca tccccactc ctgggtggtg 1500
gccgcggtga gcatctccac cgtgggctac ggagacatgt acccagagac ccacctgggc 1560

```

```

aggttttttg ccttcctctg cattgctttt gggatcattc tcaacgggat gccattttcc 1620
atcctctaca acaagttttc tgattactac agcaagctga aggcttatga gtataccacc 1680
atacgcaggg agaggggaga ggtgaacttc atgcagagag ccagaaagaa gatagctgag 1740
tgtttgcttg gaagcaaccc acagctcacc ccaagacaag agaattagta ttttatagga 1800
catgtggctg gtagattcca tgaacttcaa ggcttcattg ctcttttttt aatcattatg 1860
attggcagca aaaggaaatg tgaagcagac atacacaaag gccatttcgt tcacaaagta 1920
ctgcctctag aaatactcat tttggcccaa actcagaatg tctcatagtt gctctgtgtt 1980
gtgtgaaaca tctgaccttc tcaatgacgt tgatattgaa aacctgaggg gagcaacagc 2040
ttagattttt cttgtagctt ctcgtggcat ctagctaata aatatttttt ggacttgaaa 2100
aaa 2103

```

<210> 2
 <211> 1638
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human alpha subunit of voltage-gated potassium
 channel Kv10.1 coding sequence

<220>
 <221> CDS
 <222> (1)..(1638)
 <223> Kv10.1

```

<400> 2
atg ctc aaa cag agt gag agg aga cgg tcc tgg agc tac agg ccc tgg 48
Met Leu Lys Gln Ser Glu Arg Arg Arg Ser Trp Ser Tyr Arg Pro Trp
  1 5 10 15

aac acg acg gag aat gag ggc agc caa cac cgc agg agc att tgc tcc 96
Asn Thr Thr Glu Asn Glu Gly Ser Gln His Arg Arg Ser Ile Cys Ser
 20 25 30

ctg ggt gcc cgt tcc ggc tcc cag gcc agc atc cac ggc tgg aca gag 144
Leu Gly Ala Arg Ser Gly Ser Gln Ala Ser Ile His Gly Trp Thr Glu
 35 40 45

ggc aac tat aac tac tac atc gag gaa gac gaa gac ggg gag gag gag 192
Gly Asn Tyr Asn Tyr Tyr Ile Glu Glu Asp Glu Asp Gly Glu Glu Glu
 50 55 60

gac cag tgg aag gac gac ctg gca gaa gag gac cag cag gca ggg gag 240
Asp Gln Trp Lys Asp Asp Leu Ala Glu Glu Asp Gln Gln Ala Gly Glu
 65 70 75 80

gtc acc acc gcc aag ccc gag ggc ccc agc gac cct ccg gcc ctg ctg 288
Val Thr Thr Ala Lys Pro Glu Gly Pro Ser Asp Pro Pro Ala Leu Leu
 85 90 95

tcc acg ctg aat gtg aac gtg ggt ggc cac agc tac cag ctg gac tac 336
Ser Thr Leu Asn Val Asn Val Gly Gly His Ser Tyr Gln Leu Asp Tyr
100 105 110

tgc gag ctg gcc ggc ttc ccc aag acg cgc cta ggt cgc ctg gcc acc 384
Cys Glu Leu Ala Gly Phe Pro Lys Thr Arg Leu Gly Arg Leu Ala Thr
115 120 125

```

tcc acc agc cgc agc cgc cag cta agc ctg tgc gac gac tac gag gag Ser Thr Ser Arg Ser Arg Gln Leu Ser Leu Cys Asp Asp Tyr Glu Glu 130 135 140	432
cag aca gac gaa tac ttc ttc gac cgc gac ccg gcc gtc ttc cag ctg Gln Thr Asp Glu Tyr Phe Phe Asp Arg Asp Pro Ala Val Phe Gln Leu 145 150 155 160	480
gtc tac aat ttc tac ctg tcc ggg gtg ctg ctg gtg ctc gac ggg ctg Val Tyr Asn Phe Tyr Leu Ser Gly Val Leu Leu Val Leu Asp Gly Leu 165 170 175	528
tgt ccg cgc cgc ttc ctg gag gag ctg ggc tac tgg ggc gtg cgg ctc Cys Pro Arg Arg Phe Leu Glu Glu Leu Gly Tyr Trp Gly Val Arg Leu 180 185 190	576
aag tac acg cca cgc tgc tgc cgc atc tgc ttc gag gag cgg cgc gac Lys Tyr Thr Pro Arg Cys Cys Arg Ile Cys Phe Glu Glu Arg Arg Asp 195 200 205	624
gag ctg agc gaa cgg ctc aag atc cag cac gag ctg cgc gcg cag gcg Glu Leu Ser Glu Arg Leu Lys Ile Gln His Glu Leu Arg Ala Gln Ala 210 215 220	672
cag gtc gag gag gcg gag gaa ctc ttc cgc gac atg cgc ttc tac ggc Gln Val Glu Glu Ala Glu Glu Leu Phe Arg Asp Met Arg Phe Tyr Gly 225 230 235 240	720
ccg cag cgg cgc cgc ctc tgg aac ctc atg gag aag cca ttc tcc tcg Pro Gln Arg Arg Leu Trp Asn Leu Met Glu Lys Pro Phe Ser Ser 245 250 255	768
gtg gcc gcc aag gcc atc ggg gtg gcg tcc agc acc ttc gtg ctc gtc Val Ala Ala Lys Ala Ile Gly Val Ala Ser Ser Thr Phe Val Leu Val 260 265 270	816
tcc gtg gtg gcg ctg gcg ctc aac acc gtg gag gag atg cag cag cac Ser Val Val Ala Leu Ala Leu Asn Thr Val Glu Glu Met Gln Gln His 275 280 285	864
tcg ggg cag ggc gag ggc ggc cca gac ctg cgg ccc atc ctg gag cac Ser Gly Gln Gly Glu Gly Gly Pro Asp Leu Arg Pro Ile Leu Glu His 290 295 300	912
gtg gag atg ctg tgc atg ggc ttc ttc acg ctc gag tac ctg ctg cgc Val Glu Met Leu Cys Met Gly Phe Phe Thr Leu Glu Tyr Leu Leu Arg 305 310 315 320	960
cta gcc tcc acg ccc gac ctg agg cgc ttc gcg cgc agc gcc ctc aac Leu Ala Ser Thr Pro Asp Leu Arg Arg Phe Ala Arg Ser Ala Leu Asn 325 330 335	1008
ctg gtg gac ctg gtg gcc atc ctg ccg ctc tac ctt cag ctg ctg ctc Leu Val Asp Leu Val Ala Ile Leu Pro Leu Tyr Leu Gln Leu Leu Leu 340 345 350	1056
gag tgc ttc acg ggc gag ggc cac caa cgc ggc cag acg gtg ggc agc Glu Cys Phe Thr Gly Glu Gly His Gln Arg Gly Gln Thr Val Gly Ser 355 360 365	1104

gtg ggt aag gtg ggt cag gtg ttg cgc gtc atg cgc ctc atg cgc atc	1152
Val Gly Lys Val Gly Gln Val Leu Arg Val Met Arg Leu Met Arg Ile	
370 375 380	
ttc cgc atc ctc aag ctg gcg cgc cac tcc acc gga ctg cgt gcc ttc	1200
Phe Arg Ile Leu Lys Leu Ala Arg His Ser Thr Gly Leu Arg Ala Phe	
385 390 395 400	
ggc ttc acg ctg cgc cag tgc tac cag cag gtg ggc tgc ctg ctg ctc	1248
Gly Phe Thr Leu Arg Gln Cys Tyr Gln Gln Val Gly Cys Leu Leu Leu	
405 410 415	
ttc atc gcc atg ggc atc ttc act ttc tct gcg gct gtc tac tct gtg	1296
Phe Ile Ala Met Gly Ile Phe Thr Phe Ser Ala Ala Val Tyr Ser Val	
420 425 430	
gag cac gat gtg ccc agc acc aac ttc act acc atc ccc cac tcc tgg	1344
Glu His Asp Val Pro Ser Thr Asn Phe Thr Thr Ile Pro His Ser Trp	
435 440 445	
tgg tgg gcc gcg gtg agc atc tcc acc gtg ggc tac gga gac atg tac	1392
Trp Trp Ala Ala Val Ser Ile Ser Thr Val Gly Tyr Gly Asp Met Tyr	
450 455 460	
cca gag acc cac ctg ggc agg ttt ttt gcc ttc ctc tgc att gct ttt	1440
Pro Glu Thr His Leu Gly Arg Phe Phe Ala Phe Leu Cys Ile Ala Phe	
465 470 475 480	
ggg atc att ctc aac ggg atg ccc att tcc atc ctc tac aac aag ttt	1488
Gly Ile Ile Leu Asn Gly Met Pro Ile Ser Ile Leu Tyr Asn Lys Phe	
485 490 495	
tct gat tac tac agc aag ctg aag gct tat gag tat acc acc ata cgc	1536
Ser Asp Tyr Tyr Ser Lys Leu Lys Ala Tyr Glu Tyr Thr Thr Ile Arg	
500 505 510	
agg gag agg gga gag gtg aac ttc atg cag aga gcc aga aag aag ata	1584
Arg Glu Arg Gly Glu Val Asn Phe Met Gln Arg Ala Arg Lys Lys Ile	
515 520 525	
gct gag tgt ttg ctt gga agc aac cca cag ctc acc cca aga caa gag	1632
Ala Glu Cys Leu Leu Gly Ser Asn Pro Gln Leu Thr Pro Arg Gln Glu	
530 535 540	
aat tag	1638
Asn	
545	

<210> 3

<211> 545

<212> PRT

<213> Homo sapiens

<223> human alpha subunit of voltage-gated potassium
channel Kv10.1

<220>

<221> PEPTIDE

<222> (102)..(514)

<223> conserved region of voltage-gated potassium
channel Kv10.1

Met 1	Leu	Lys	Gln	Ser 5	Glu	Arg	Arg	Arg	Ser 10	Trp	Ser	Tyr	Arg	Pro 15	Trp
Asn	Thr	Thr	Glu	Asn	Glu	Gly	Ser	Gln	His	Arg	Arg	Ser	Ile	Cys 20	Ser
Leu	Gly	Ala	Arg	Ser	Gly	Ser	Gln	Ala	Ser	Ile	His	Gly	Trp	Thr	Glu
Gly	Asn	Tyr	Asn	Tyr	Tyr	Ile	Glu	Glu	Asp	Glu	Asp	Gly	Glu	Glu	Glu
Asp	Gln	Trp	Lys	Asp	Asp	Leu	Ala	Glu	Glu	Asp	Gln	Gln	Ala	Gly	Glu
Val	Thr	Thr	Ala	Lys	Pro	Glu	Gly	Pro	Ser	Asp	Pro	Pro	Ala	Leu	Leu
Ser	Thr	Leu	Asn	Val	Asn	Val	Gly	Gly	His	Ser	Tyr	Gln	Leu	Asp	Tyr
Cys	Glu	Leu	Ala	Gly	Phe	Pro	Lys	Thr	Arg	Leu	Gly	Arg	Leu	Ala	Thr
Ser	Thr	Ser	Arg	Ser	Arg	Gln	Leu	Ser	Leu	Cys	Asp	Asp	Tyr	Glu	Glu
Gln	Thr	Asp	Glu	Tyr	Phe	Phe	Asp	Arg	Asp	Pro	Ala	Val	Phe	Gln	Leu
Val	Tyr	Asn	Phe	Tyr	Leu	Ser	Gly	Val	Leu	Leu	Val	Leu	Asp	Gly	Leu
Cys	Pro	Arg	Arg	Phe	Leu	Glu	Glu	Leu	Gly	Tyr	Trp	Gly	Val	Arg	Leu
Lys	Tyr	Thr	Pro	Arg	Cys	Cys	Arg	Ile	Cys	Phe	Glu	Glu	Arg	Arg	Asp
Glu	Leu	Ser	Glu	Arg	Leu	Lys	Ile	Gln	His	Glu	Leu	Arg	Ala	Gln	Ala
Gln	Val	Glu	Glu	Ala	Glu	Glu	Leu	Phe	Arg	Asp	Met	Arg	Phe	Tyr	Gly
Pro	Gln	Arg	Arg	Arg	Leu	Trp	Asn	Leu	Met	Glu	Lys	Pro	Phe	Ser	Ser
Val	Ala	Ala	Lys	Ala	Ile	Gly	Val	Ala	Ser	Ser	Thr	Phe	Val	Leu	Val
Ser	Val	Val	Ala	Leu	Ala	Leu	Asn	Thr	Val	Glu	Glu	Met	Gln	Gln	His
Ser	Gly	Gln	Gly	Glu	Gly	Gly	Pro	Asp	Leu	Arg	Pro	Ile	Leu	Glu	His
Val	Glu	Met	Leu	Cys	Met	Gly	Phe	Phe	Thr	Leu	Glu	Tyr	Leu	Leu	Arg
Leu	Ala	Ser	Thr	Pro	Asp	Leu	Arg	Arg	Phe	Ala	Arg	Ser	Ala	Leu	Asn
Leu	Val	Asp	Leu	Val	Ala	Ile	Leu	Pro	Leu	Tyr	Leu	Gln	Leu	Leu	Leu
Glu	Cys	Phe	Thr	Gly	Glu	Gly	His	Gln	Arg	Gly	Gln	Thr	Val	Gly	Ser
Val	Gly	Lys	Val	Gly	Gln	Val	Leu	Arg	Val	Met	Arg	Leu	Met	Arg	Ile
Phe	Arg	Ile	Leu	Lys	Leu	Ala	Arg	His	Ser	Thr	Gly	Leu	Arg	Ala	Phe
Gly	Phe	Thr	Leu	Arg	Gln	Cys	Tyr	Gln	Gln	Val	Gly	Cys	Leu	Leu	Leu
Phe	Ile	Ala	Met	Gly	Ile	Phe	Thr	Phe	Ser	Ala	Ala	Val	Tyr	Ser	Val
Glu	His	Asp	Val	Pro	Ser	Thr	Asn	Phe	Thr	Thr	Ile	Pro	His	Ser	Trp
Trp	Trp	Ala	Ala	Val	Ser	Ile	Ser	Thr	Val	Gly	Tyr	Gly	Asp	Met	Tyr
Pro	Glu	Thr	His	Leu	Gly	Arg	Phe	Phe	Ala	Phe	Leu	Cys	Ile	Ala	Phe

Gly Ile Ile Leu Asn Gly Met Pro Ile Ser Ile Leu Tyr Asn Lys Phe
 485 490 495
 Ser Asp Tyr Tyr Ser Lys Leu Lys Ala Tyr Glu Tyr Thr Thr Ile Arg
 500 505 510
 Arg Glu Arg Gly Glu Val Asn Phe Met Gln Arg Ala Arg Lys Lys Ile
 515 520 525
 Ala Glu Cys Leu Leu Gly Ser Asn Pro Gln Leu Thr Pro Arg Gln Glu
 530 535 540
 Asn
 545

<210> 4
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense Oligo 1

<400> 4
 gccatgctca aacagagtga gaggagac 28

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:antisense Oligo
 2

<400> 5
 gagcgtgaag aagcccatgc acag 24

<210> 6
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:RACE PCR
 gene-specific antisense Oligo 3

<400> 6
 gcagcaccctt ggacaggttag aaa 23

<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:nested
 gene-specific antisense Oligo 4

<400> 7
 cgcccggttc gcggtcgaag aagt 24

<210> 8
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:standard 3'
 RACE PCR nested Oligo 5

 <400> 8
 ccaccatgag ggcagccaac accgcaggag ca 32

 <210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:new 3' RACE
 gene-specific sense Oligo 6

 <400> 9
 ggctgtctac tctgtggagc acgat 25

 <210> 10
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:antisense Oligo
 7

 <400> 10
 gagtatttct agaggcagta ctttgtg 27

 <210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:coding region
 Oligo 8

 <400> 11
 attctcttgt cttgggggtga gctg 24

 <210> 12
 <211> 854
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human voltage-gated potassium channel Kv2.1

<400> 12

Met	Thr	Lys	His	Gly	Ser	Arg	Ser	Thr	Ser	Ser	Leu	Pro	Pro	Glu	Pro
1				5					10					15	
Met	Glu	Ile	Val	Arg	Ser	Lys	Ala	Cys	Ser	Arg	Arg	Val	Arg	Leu	Asn
			20					25					30		
Val	Gly	Gly	Leu	Ala	His	Glu	Val	Leu	Trp	Arg	Thr	Leu	Asp	Arg	Leu
		35						40				45			
Pro	Arg	Thr	Arg	Leu	Gly	Lys	Leu	Arg	Asp	Cys	Asn	Thr	His	Asp	Ser
	50					55					60				
Leu	Leu	Glu	Val	Cys	Asp	Tyr	Ser	Leu	Asp	Asp	Asn	Glu	Tyr	Phe	
65					70				75					80	
Phe	Asp	Arg	His	Pro	Gly	Ala	Phe	Thr	Ser	Ile	Leu	Asn	Phe	Tyr	Arg
			85					90						95	
Thr	Gly	Arg	Leu	His	Met	Met	Glu	Glu	Met	Cys	Ala	Leu	Ser	Phe	Ser
			100					105					110		
Gln	Glu	Leu	Asp	Tyr	Trp	Gly	Ile	Asp	Glu	Ile	Tyr	Leu	Glu	Ser	Cys
		115					120					125			
Cys	Gln	Ala	Arg	Tyr	His	Gln	Lys	Lys	Glu	Gln	Met	Asn	Glu	Glu	Leu
	130					135					140				
Lys	Arg	Glu	Ala	Glu	Thr	Leu	Arg	Glu	Arg	Glu	Gly	Glu	Glu	Phe	Asp
145					150				155					160	
Asn	Thr	Cys	Cys	Ala	Glu	Lys	Arg	Lys	Lys	Leu	Trp	Asp	Leu	Leu	Glu
			165					170					175		
Lys	Pro	Asn	Ser	Ser	Val	Ala	Ala	Lys	Ile	Leu	Ala	Ile	Ile	Ser	Ile
		180						185					190		
Met	Phe	Ile	Val	Leu	Ser	Thr	Ile	Ala	Leu	Ser	Leu	Asn	Thr	Leu	Pro
	195					200						205			
Glu	Leu	Gln	Ser	Leu	Asp	Glu	Phe	Gly	Gln	Ser	Thr	Asp	Asn	Pro	Gln
	210					215					220				
Leu	Ala	His	Val	Glu	Ala	Val	Cys	Ile	Ala	Trp	Phe	Thr	Met	Glu	Tyr
225					230				235					240	
Leu	Leu	Arg	Phe	Leu	Ser	Ser	Pro	Lys	Lys	Trp	Lys	Phe	Phe	Lys	Gly
			245					250					255		
Pro	Leu	Asn	Ala	Ile	Asp	Leu	Leu	Ala	Ile	Leu	Pro	Tyr	Tyr	Val	Thr
		260						265					270		
Ile	Phe	Leu	Thr	Glu	Ser	Asn	Lys	Ser	Val	Leu	Gln	Phe	Gln	Asn	Val
	275					280						285			
Arg	Arg	Val	Val	Gln	Ile	Phe	Arg	Ile	Met	Arg	Ile	Leu	Arg	Ile	Leu
	290					295					300				
Lys	Leu	Ala	Arg	His	Ser	Thr	Gly	Leu	Gln	Ser	Leu	Gly	Phe	Thr	Leu
305					310					315				320	
Arg	Arg	Ser	Tyr	Asn	Glu	Leu	Gly	Leu	Leu	Ile	Leu	Phe	Leu	Ala	Met
			325					330					335		
Gly	Ile	Met	Ile	Phe	Ser	Ser	Leu	Val	Phe	Phe	Ala	Glu	Lys	Asp	Glu
		340					345					350			
Asp	Asp	Thr	Lys	Phe	Lys	Ser	Ile	Pro	Ala	Ser	Phe	Trp	Trp	Ala	Thr
	355					360						365			
Ile	Thr	Met	Thr	Thr	Val	Gly	Tyr	Gly	Asp	Ile	Tyr	Pro	Lys	Thr	Leu
	370					375					380				
Leu	Gly	Lys	Ile	Val	Gly	Gly	Leu	Cys	Cys	Ile	Ala	Gly	Val	Leu	Val
385					390					395				400	
Ile	Ala	Leu	Pro	Ile	Pro	Ile	Ile	Val	Asn	Asn	Phe	Ser	Glu	Phe	Tyr
			405						410				415		
Lys	Glu	Gln	Lys	Arg	Gln	Glu	Lys	Ala	Ile	Lys	Arg	Arg	Glu	Ala	Leu
		420						425					430		
Glu	Arg	Ala	Lys	Arg	Asn	Gly	Ser	Ile	Val	Ser	Met	Asn	Met	Lys	Asp
	435					440					445				
Ala	Phe	Ala	Arg	Ser	Ile	Glu	Met	Met	Asp	Ile	Val	Val	Glu	Lys	Asn
	450					455					460				
Gly	Glu	Asn	Met	Gly	Lys	Lys	Asp	Lys	Val	Gln	Asp	Asn	His	Leu	Ser
465					470					475				480	

Pro Asn Lys Trp Lys Trp Thr Lys Arg Thr Leu Ser Glu Thr Ser Ser
 485 490 495
 Ser Lys Ser Phe Glu Thr Lys Glu Gln Gly Ser Pro Glu Lys Ala Arg
 500 505 510
 Ser Ser Ser Ser Pro Gln His Leu Asn Val Gln Gln Leu Glu Asp Met
 515 520 525
 Tyr Asn Lys Met Ala Lys Thr Gln Ser Gln Pro Ile Leu Asn Thr Lys
 530 535 540
 Glu Ser Ala Ala Gln Ser Lys Pro Lys Glu Glu Leu Glu Met Glu Ser
 545 550 555 560
 Ile Pro Ser Pro Val Ala Pro Leu Pro Thr Arg Thr Glu Gly Val Ile
 565 570 575
 Asp Met Arg Ser Met Ser Ser Ile Asp Ser Phe Ile Ser Cys Ala Thr
 580 585 590
 Asp Phe Pro Glu Ala Thr Arg Phe Ser His Ser Pro Leu Thr Ser Leu
 595 600 605
 Pro Ser Lys Thr Gly Gly Ser Thr Ala Pro Glu Val Gly Trp Arg Gly
 610 615 620
 Ala Leu Gly Ala Ser Gly Gly Arg Phe Val Glu Ala Asn Pro Ser Pro
 625 630 635 640
 Asp Ala Ser Gln His Ser Ser Phe Phe Ile Glu Ser Pro Lys Ser Ser
 645 650 655
 Met Lys Thr Asn Asn Pro Leu Lys Leu Arg Ala Leu Lys Val Asn Phe
 660 665 670
 Met Glu Gly Asp Pro Ser Pro Leu Leu Pro Val Leu Gly Met Tyr His
 675 680 685
 Asp Pro Leu Arg Asn Arg Gly Ser Ala Ala Ala Val Ala Gly Leu
 690 695 700
 Glu Cys Ala Thr Leu Leu Asp Lys Ala Val Leu Ser Pro Glu Ser Ser
 705 710 715 720
 Ile Tyr Thr Thr Ala Ser Ala Lys Thr Pro Pro Arg Ser Pro Glu Lys
 725 730 735
 His Thr Ala Ile Ala Phe Asn Phe Glu Ala Gly Val His Gln Tyr Ile
 740 745 750
 Asp Ala Asp Thr Asp Asp Glu Gly Gln Leu Leu Tyr Ser Val Asp Ser
 755 760 765
 Ser Pro Pro Lys Ser Leu Pro Gly Ser Thr Ser Pro Lys Phe Ser Thr
 770 775 780
 Gly Thr Arg Ser Glu Lys Asn His Phe Glu Ser Ser Pro Leu Pro Thr
 785 790 795 800
 Ser Pro Lys Phe Leu Arg Gln Asn Cys Ile Tyr Ser Thr Glu Ala Leu
 805 810 815
 Thr Gly Lys Gly Pro Ser Gly Gln Glu Lys Cys Lys Leu Glu Asn His
 820 825 830
 Ile Ser Pro Asp Val Arg Val Leu Pro Gly Gly Gly Ala His Gly Ser
 835 840 845
 Thr Arg Asp Gln Ser Ile
 850

<210> 13

<211> 806

<212> PRT

<213> Homo sapiens

<220>

<223> human voltage-gated potassium channel Kv2.2

<400> 13

Met Ala Glu Lys Ala Pro Pro Gly Leu Asn Arg Lys Thr Ser Arg Ser
 1 5 10 15

Thr	Leu	Ser	Leu	Pro	Pro	Glu	Pro	Val	Asp	Ile	Ile	Arg	Ser	Lys	Thr	20	25	30
Cys	Ser	Arg	Arg	Val	Lys	Ile	Asn	Val	Gly	Gly	Leu	Asn	His	Glu	Val	35	40	45
Leu	Trp	Arg	Thr	Leu	Asp	Arg	Leu	Pro	Arg	Thr	Arg	Leu	Gly	Lys	Leu	50	55	60
Arg	Asp	Cys	Asn	Thr	His	Glu	Ser	Leu	Leu	Glu	Val	Cys	Asp	Asp	Tyr	65	70	75
Asn	Leu	Asn	Glu	Asn	Glu	Tyr	Phe	Phe	Asp	Arg	His	Pro	Gly	Ala	Phe	85	90	95
Thr	Ser	Ile	Leu	Asn	Phe	Tyr	Arg	Thr	Gly	Lys	Leu	His	Met	Met	Glu	100	105	110
Glu	Met	Cys	Ala	Leu	Ser	Phe	Gly	Gln	Glu	Leu	Asp	Tyr	Trp	Gly	Ile	115	120	125
Asp	Glu	Ile	Tyr	Leu	Glu	Ser	Cys	Cys	Gln	Ala	Arg	Tyr	His	Gln	Lys	130	135	140
Lys	Glu	Gln	Met	Asn	Glu	Glu	Leu	Arg	Arg	Glu	Ala	Glu	Thr	Met	Arg	145	150	155
Asp	Gly	Glu	Gly	Glu	Phe	Asp	Asn	Thr	Cys	Cys	Pro	Asp	Lys	Arg		165	170	175
Lys	Lys	Leu	Trp	Asp	Leu	Leu	Glu	Lys	Pro	Asn	Ser	Ser	Val	Ala	Ala	180	185	190
Lys	Ile	Leu	Ala	Ile	Val	Ser	Ile	Leu	Phe	Ile	Val	Leu	Ser	Thr	Ile	195	200	205
Ala	Leu	Ser	Leu	Asn	Thr	Leu	Pro	Glu	Leu	Gln	Glu	Thr	Asp	Glu	Phe	210	215	220
Gly	Gln	Leu	Asn	Asp	Asn	Arg	Gln	Leu	Ala	His	Val	Glu	Ala	Val	Cys	225	230	235
Ile	Ala	Trp	Phe	Thr	Met	Glu	Tyr	Leu	Leu	Arg	Phe	Leu	Ser	Ser	Pro	245	250	255
Asn	Lys	Trp	Lys	Phe	Phe	Lys	Gly	Pro	Leu	Asn	Val	Ile	Asp	Leu	Leu	260	265	270
Ala	Ile	Leu	Pro	Tyr	Tyr	Val	Thr	Ile	Phe	Leu	Thr	Glu	Ser	Asn	Lys	275	280	285
Ser	Val	Leu	Gln	Phe	Gln	Asn	Val	Arg	Arg	Val	Val	Gln	Ile	Phe	Arg	290	295	300
Ile	Met	Arg	Ile	Leu	Arg	Ile	Leu	Lys	Leu	Ala	Arg	His	Ser	Thr	Gly	305	310	315
Leu	Gln	Ser	Leu	Gly	Phe	Thr	Leu	Arg	Arg	Ser	Tyr	Asn	Glu	Leu	Gly	325	330	335
Leu	Leu	Ile	Leu	Phe	Leu	Ala	Met	Gly	Ile	Met	Ile	Phe	Ser	Ser	Leu	340	345	350
Val	Phe	Phe	Ala	Glu	Lys	Asp	Glu	Asp	Ala	Thr	Lys	Phe	Thr	Ser	Ile	355	360	365
Pro	Ala	Ser	Phe	Trp	Trp	Ala	Thr	Ile	Thr	Met	Thr	Thr	Val	Gly	Tyr	370	375	380
Gly	Asp	Ile	Tyr	Pro	Lys	Thr	Leu	Leu	Gly	Lys	Ile	Val	Gly	Gly	Leu	385	390	395
Cys	Cys	Ile	Ala	Gly	Val	Leu	Val	Ile	Ala	Leu	Pro	Ile	Pro	Ile	Ile	405	410	415
Val	Asn	Asn	Phe	Ser	Glu	Phe	Tyr	Lys	Glu	Gln	Lys	Arg	Gln	Glu	Lys	420	425	430
Ala	Ile	Lys	Arg	Arg	Glu	Ala	Leu	Glu	Arg	Ala	Lys	Arg	Asn	Gly	Ser	435	440	445
Ile	Val	Ser	Met	Asn	Leu	Lys	Asp	Ala	Phe	Ala	Arg	Ser	Met	Glu	Leu	450	455	460
Ile	Asp	Val	Ala	Val	Glu	Lys	Ala	Gly	Glu	Ser	Ala	Asn	Thr	Lys	Asp	465	470	475
Ser	Ala	Asp	Asp	Asn	His	Leu	Ser	Pro	Ser	Arg	Trp	Lys	Trp	Ala	Arg	485	490	495

Lys Ala Leu Ser Glu Thr Ser Ser Asn Lys Ser Phe Glu Asn Lys Tyr
 500 505 510
 Gln Glu Val Ser Gln Lys Asp Ser His Glu Gln Leu Asn Asn Thr Phe
 515 520 525
 Ser Ser Ser Pro Gln His Leu Ser Ala Gln Lys Leu Glu Met Leu Tyr
 530 535 540
 Asn Glu Ile Thr Lys Thr Gln Pro His Ser His Pro Asn Pro Asp Cys
 545 550 555 560
 Gln Glu Lys Pro Glu Arg Pro Ser Ala Tyr Glu Glu Glu Ile Glu Met
 565 570 575
 Glu Glu Val Val Cys Pro Gln Glu Gln Leu Ala Val Ala Gln Thr Glu
 580 585 590
 Val Ile Val Asp Met Lys Ser Thr Ser Ser Ile Asp Ser Phe Thr Ser
 595 600 605
 Cys Ala Thr Asp Phe Thr Glu Thr Glu Arg Ser Pro Leu Pro Pro Pro
 610 615 620
 Ser Ala Ser His Leu Gln Met Lys Phe Pro Thr Asp Leu Pro Gly Thr
 625 630 635 640
 Glu Glu His Gln Arg Ala Arg Gly Pro Phe Leu Thr Leu Ser Arg
 645 650 655
 Glu Lys Gly Pro Ala Ala Arg Asp Gly Thr Leu Glu Tyr Ala Pro Val
 660 665 670
 Asp Ile Thr Val Asn Leu Asp Ala Ser Gly Ser Gln Cys Gly Leu His
 675 680 685
 Ser Pro Leu Gln Ser Asp Asn Ala Thr Asp Ser Pro Lys Ser Ser Leu
 690 695 700
 Lys Gly Ser Asn Pro Leu Lys Ser Arg Ser Leu Lys Val Asn Phe Lys
 705 710 715 720
 Glu Asn Arg Gly Ser Ala Pro Gln Thr Pro Pro Ser Thr Ala Arg Pro
 725 730 735
 Leu Pro Val Thr Thr Ala Asp Phe Ser Leu Thr Thr Pro Gln His Ile
 740 745 750
 Ser Thr Ile Leu Leu Glu Glu Thr Pro Ser Gln Gly Asp Arg Pro Cys
 755 760 765
 Trp Ala Leu Arg Phe Gln Arg Leu Val Arg Asp Leu Pro Lys Gly Cys
 770 775 780
 Pro Pro Gly Phe Pro Ser Arg Asn Cys Ser Leu Ser Leu Gln Glu Arg
 785 790 795 800
 Gly Gly Ala Ser Leu Lys
 805

<210> 14

<211> 26

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(26)

<223> S6 domain of voltage-gated potassium channel
Kv10.1

<400> 14

Phe Phe Ala Phe Leu Cys Ile Ala Phe Gly Ile Ile Leu Asn Gly Met
 1 5 10 15

Pro Ile Ser Ile Leu Tyr Asn Lys Phe Ser
 20 25

<210> 15
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (1)..(26)
<223> S6 domain of voltage-gated potassium channel Kv6.1

<400> 15
Val Val Ala Leu Ser Ser Ile Leu Ser Gly Ile Leu Leu Met Ala Phe
1 5 10 15
Pro Val Thr Ser Ile Phe His Thr Phe Ser
20 25

<210> 16
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (1)..(26)
<223> S6 domain of voltage-gated potassium channel Kv2.1

<400> 16
Ile Val Gly Gly Leu Cys Cys Ile Ala Gly Val Leu Val Ile Ala Leu
1 5 10 15
Pro Ile Pro Ile Ile Val Asn Asn Phe Ser
20 25

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Kv10.1-specific
amplification primer

<400> 17
tgggctgcct gctgctcttc at 22

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Kv10.1-specific
amplification primer

<400> 18
ctctcccttc tccctgcgta tggc 24